

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Donnelly, John J  
Dwarki, Varavani J  
Liu, Margaret A  
Montgomery, Donna L  
Parker, Suezanne E  
Shiver, John W

(ii) TITLE OF INVENTION: Nucleic Acid Pharmaceuticals - Influenza  
Matrix

(iii) NUMBER OF SEQUENCES: 64

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Christine E. Carty  
(B) STREET: 126 E. Lincoln Ave., P.O. Box 2000  
(C) CITY: Rahway  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07065-0907

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/461,268  
(B) FILING DATE: 5-June-1995  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/032,383  
(B) FILING DATE: 18-May-1993

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Carty, Christine E.  
(B) REGISTRATION NUMBER: 36,099  
(C) REFERENCE/DOCKET NUMBER: 18972PIE

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908)594-6734  
(B) TELEFAX: (908)594-4720

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGTGCACCT CAAGCTGG

18

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCTTTGAGA ATGTTGCACA TTC

23

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTACAAGAT CTACCATGCT TCTAACCGAG GTC

33

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCACATAGAT CTCACCTTGA ACCGTTGCAT CTGCAC

36

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTATATAAGC AGAGCTCGTT TAG

23

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTAGCAAAGA TCTAAGGACG GTGACTGCAG

30

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTATGTGTCT GAAAATGAGC GTGGAGATTG GGCTCGCAC

39

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCGAGCCC AATCTCCACG CTCATTTTCA GACACATAC

39

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Tyr Gln Arg Thr Arg Ala Leu Val  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGTCCCG GAGACGGTCA	60
CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG	120
TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC	180
ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGATTGG	240
CTATTGGCCA TTGCATACGT TGTATCCATA TCATAATATG TACATTTATA TTGGCTCATG	300
TCCAACATTA CCGCCATGTT GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC	360
GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCGCGTT ACATAACTTA CGGTAAATGG	420
CCCGCCTGGC TGACCGCCCA ACGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC	480
CATAGTAACG CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC	540
TGCCCCACTG GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA TTGACGTCAA	600
TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG ACCTTATGGG ACTTTCCTAC	660
TTGGCAGTAC ATCTACGTAT TAGTCATCGC TATTACCATG GTGATGCGGT TTTGGCAGTA	720
CATCAATGGG CGTGGATAGC GGTTTGACTC ACGGGGATTT CCAAGTCTCC ACCCCATTGA	780
CGTCAATGGG AGTTTGTFFF GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA	840
CTCCGCCCCA TTGACGCAA TGGGCGGTAG GCGTGTACGG TGGGAGGTCT ATATAAGCAG	900
AGCTCGTTTA GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT TTGACCTCCA	960

TAGAAGACAC	CGGGACCGAT	CCAGCCTCCG	CGGCCGGGAA	CGGTGCATTG	GAACGCGGAT	1020
TCCCCGTGCC	AAGAGTGACG	TAAGTACCGC	CTATAGAGTC	TATAGGCCCA	CCCCCTTGCC	1080
TTCTTATGCA	TGCTATACTG	TTTTTGGCTT	GGGGTCTATA	CACCCCCGCT	TCCTCATGTT	1140
ATAGGTGATG	GTATAGCTTA	GCCTATAGGT	GTGGGTTATT	GACCATTATT	GACCACTCCC	1200
CTATTGGTGA	CGATACTTTC	CATTACTAAT	CCATAACATG	GCTCTTTGCC	ACAACTCTCT	1260
TTATTGGCTA	TATGCCAATA	CACTGTCCTT	CAGAGACTGA	CACGGACTCT	GTATTTTAC	1320
AGGATGGGGT	CTCATTTATT	ATTTACAAAT	TCACATATAC	AACACCACCG	TCCCCAGTGC	1380
CCGCAGTTTT	TATTAAACAT	AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCGGG	1440
ACATGGGCTC	TTCTCCGGTA	GCGGCGGAGC	TTCTACATCC	GAGCCCTGCT	CCCATGCCTC	1500
CAGCGACTCA	TGGTCGCTCG	GCAGCTCCTT	GTCCTAACA	GTGGAGGCCA	GACTTAGGCA	1560
CAGCACGATG	CCCACCACCA	CCAGTGTGCC	GCACAAGGCC	GTGGCGGTAG	GGTATGTGTC	1620
TGAAAATGAG	CTCGGGGAGC	GGGCTTGAC	CGCTGACGCA	TTTGAAGAC	TTAAGGCAGC	1680
GGCAGAAGAA	GATGCAGGCA	GCTGAGTTGT	TGTGTTCTGA	TAAGAGTCAG	AGGTAACTCC	1740
CGTTGCGGTG	CTGTTAACGG	TGGAGGGCAG	TGTAGTCTGA	GCAGTACTCG	TTGCTGCCGC	1800
GCGCGCCACC	AGACATAATA	GCTGACAGAC	TAACAGACTG	TTCTTTCCA	TGGGTCTTTT	1860
CTGCAGTCAC	CGTCCTTAGA	TCTGCTGTGC	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	1920
CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	1980
ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	2040
GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	2100
GCTCTATGGG	TACCCAGGTG	CTGAAGAATT	GACCCGGTTC	CTCCTGGGCC	AGAAAGAAGC	2160
AGGCACATCC	CCTTCTCTGT	GACACACCCT	GTCCACGCCC	CTGGTTCTTA	GTTCCAGCCC	2220
CACTCATAGG	AACTCATAG	CTCAGGAGGG	CTCCGCCTTC	AATCCCACCC	GCTAAAGTAC	2280
TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGTGG	2340
GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAATGC	CTCCAACATG	2400
TGAGGAAGTA	ATGAGAGAAA	TCATAGAATT	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	2460
CGCTCGGTG	TTCGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	2520
TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2580
AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	2640
CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2700

CAGGCGTTTC CCCCTGGAAG CTCCTCGTG CGCTCTCCTG TTCCGACCCT GCCGCTTACC	2760
GGATACCTGT CCGCCTTTCT CCCTTCGGGA AGCGTGGCGC TTTCTCAATG CTCACGCTGT	2820
AGGTATCTCA GTTCGGTGTA GGTGTTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC	2880
GTTACAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA CCCGGTAAGA	2940
CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC GAGGTATGTA	3000
GGCGGTGCTA CAGAGTTCTT GAAGTGGTGG CCTAACTACG GCTACACTAG AAGGACAGTA	3060
TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA	3120
TCCGGCAAAC AAACCACCGC TGGTAGCGGT GGTTTTTTTT TTTGCAAGCA GCAGATTACG	3180
CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC TGACGCTCAG	3240
TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAAG GATCTTCACC	3300
TAGATCCTTT TAAATTAAAA ATGAAGTTTT AAATCAATCT AAAGTATATA TGAGTAACT	3360
TGGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT	3420
CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA	3480
CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC TCCAGATTTA	3540
TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC AACTTTATCC	3600
GCCTCCATCC AGTCTATTAA TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT	3660
AGTTTGCGCA ACGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT	3720
ATGGCTTCAT TCAGTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG	3780
TGCAAAAAAG CGGTTAGCTC CTTCCGTCCT CCGATCGTTG TCAGAAGTAA GTTGGCCGCA	3840
GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC TTACTGTCAT GCCATCCGTA	3900
AGATGCTTTT CTGTGACTGG TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG	3960
CGACCGAGTT GCTCTTGCCC GCGTCAATA CGGGATAATA CCGCGCCACA TAGCAGAACT	4020
TTAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG	4080
CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC AGCATCTTTT	4140
ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC AAAAAAGGGA	4200
ATAAGGGCGA CACGGAAATG TTGAATACTC ATACTCTTCC TTTTTCATA TTATTGAAGC	4260
ATTTATCAGG GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA	4320
CAAATAGGGG TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CTGACGTCTA AGAAACCATT	4380

ATTATCATGA CATTAACCTA TAAAAATAGG CGTATCACGA GGCCCTTTCG TC

4432

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both.

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTGGCTATT GGCCATTGCA TACGTTGTAT CCATATCATA ATATGTACAT TTATATTGGC	60
TCATGTCCAA CATTACCGCC ATGTTGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA	120
ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA ACTTACGGTA	180
AATGGCCCGC CTGGCTGACC GCCCAACGAC CCCCGCCCAT TGACGTCAAT AATGACGTAT	240
GTTCCCATAG TAACGCCAAT AGGGACTTTC CATTGACGTC AATGGGTGGA GTATTTACGG	300
TAAACTGCCC ACTTGGCAGT ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC	360
GTCAATGACG GTAAATGGCC CGCCTGGCAT TATGCCAGT ACATGACCTT ATGGGACTTT	420
CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGTGAT GCGGTTTTGG	480
CAGTACATCA ATGGGCGTGG ATAGCGGTTT GACTCACGGG GATTTCCAAG TCTCCACCCC	540
ATTGACGTCA ATGGGAGTTT GTTTTGGCAC CAAAATCAAC GGGACTTTCC AAAATGTCGT	600
AACAACCTCCG CCCCATTGAC GCAAATGGGC GGTAGGCGTG TACGGTGGGA GGTCTATATA	660
AGCAGAGCTC GTTTAGTGAA CCGTCAGATC GCCTGGAGAC GCCATCCACG CTGTTTTGAC	720
CTCCATAGAA GACACCGGGA CCGATCCAGC CTCCGCGGCC GGGAACGGTG CATTGGAACG	780
CGGATTCCCC GTGCCAAGAG TGACGTAAGT ACCGCCTATA GAGTCTATAG GCCCACCCCC	840
TTGGCTTCTT ATGCATGCTA TACTGTTTTT GGCTTGGGGT CTATACACCC CCGCTTCCTC	900
ATGTTATAGG TGATGGTATA GCTTAGCCTA TAGGTGTGGG TTATTGACCA TTATTGACCA	960
CTCCCCTATT GGTGACGATA CTTTCCATTA CTAATCCATA ACATGGCTCT TTGCCACAAC	1020
TCTCTTTATT GGCTATATGC CAATACACTG TCCTTCAGAG ACTGACACGG ACTCTGTATT	1080



```

TTTACAGGAT GGGGTCTCAT TTATTATTTA CAAATTCACA TATACAACAC CACCGTCCCC 1140
AGTGCCCGCA GTTTTTATTA AACATAACGT GGGATCTCCA CGCGAATCTC GGGTACGTGT 1200
TCCGGACATG GGCTCTTCTC CGGTAGCGGC GGAGCTTCTA CATCCGAGCC CTGCTCCCAT 1260
GCCTCCAGCG ACTCATGGTC GCTCGGCAGC TCCTTGCTCC TAACAGTGGA GGCCAGACTT 1320
AGGCACAGCA CGATGCCCCAC CACCACCAGT GTGCCGCACA AGGCCGTGGC GGTAGGGTAT 1380
GTGTCTGAAA ATGAGCTCGG GGAGCGGGCT TGCACCGCTG ACGCATTTGG AAGACTTAAG 1440
GCAGCGGCAG AAGAAGATGC AGGCAGCTGA GTTGTGTGT TCTGATAAGA GTCAGAGGTA 1500
ACTCCCGTTG CGGTGCTGTT AACGGTGGAG GGCAGTGTAG TCTGAGCAGT ACTCGTTGCT 1560
GCCGCGCGCG CCACCAGACA TAATAGCTGA CAGACTAACA GACTGTCCTT TTCCATGGGT 1620
CTTTTCTGCA GTCACCGTCC TTAGATCTGC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT 1680
TTGCCCCCTCC CCCGTGCCTT CCTTGACCCT GGAAGGTGCC ACTCCCCTG TCCTTTCCTA 1740
ATAAAATGAG GAAATTGCAT CGCATTGTCT GAGTAGGTGT CATTCTATTC TGGGGGGTGG 1800
GGTGGGGCAG CACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG CTGGGGATGC 1860
GGTGGGCTCT ATGGGTACCC AGGTGCTGAA GAATTGACCC GGTTCCTCCT GGGCCAGAAA 1920
GAAGCAGGCA CATCCCCTTC TCTGTGACAC ACCCTGTCCA CGCCCCTGGT TCTTAGTTCC 1980
AGCCCCACTC ATAGGACACT CATAGCTCAG GAGGGCTCCG CCTTCAATCC CACCCGCTAA 2040
AGTACTTGGA GCGGTCTCTC CCTCCCTCAT CAGCCCACCA AACCAAACCT AGCCTCCAAG 2100
AGTGGAAGA AATTAAAGCA AGATAGGCTA TTAAGTGCAG AGGGAGAGAA AATGCCTCCA 2160
ACATGTGAGG AAGTAATGAG AGAAATCATA GAATTC 2196

```

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCACCGTCC TTAGATCAAT TCCAGCAAAA GCAGGGTAGA TAATCACTCA CTGAGTGACA 60  
TCAAAATCAT G 71

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 117 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCGTCCTTA GATCAGCTTG GCAAAAGCAG GCAAACCATT TGAATGGATG TCAATCCGAC 60  
CTTACTTTTC TTAAAAGTGC CAGCACAAAA TGCTATAAGC ACAACTTTCC CTTATAC 117

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 136 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTCACCGTCC TTAGATCAAT TCCAGCAAAA GCAGGGTGAC AAAACATAA TGGATCCAAA 60  
CACTGTGTCA AGCTTTCAGG TAGATTGCTT TCTTTGGCAT GTCCGCAAAC GAGTTGCAGA 120  
CCAAGAACTA GGTGAT 136

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
TCTGCAGTCA CCGTCCTTAG ATCAGCTTGG AGCAAAAGCA GGGGAAAATA AAAACAACCA      60
AAATGAAGGC AAACCTACTG GTCCTGTAA GTGCACTTGC AGCTGCAGAT GCAGACACAA      120
TATGTATAGG CTACCATGCG AACAATTCAA CC                                     152
```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 162 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
TTTTCTGCAG TCACCGTCCT TAGATCCCGA ATTCCAGCAA AAGCAGGTCA ATTATATTCA      60
ATATGGAAAG AATAAAAGAA CTAAGAAATC TAATGTCGCA GTCTGCCACC CCGGAGATAC      120
TCACAAAAAC CACCGTGGAC CATATGGCCA TAATCAAGAA GT                                     162
```

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 122 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCACCGTCC TTAGATCTAC CATGAGTCTT CTAACCGAGG TCGAAACGTA CGTACTCTCT	60
ATCATCCCGT CAGGCCCCCT CAAAGCCGAG ATCGCACAGA GACTTGAAGA GTTGACGGAA	120
GA	122

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA	60
CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG	120
TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC	180
ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGATTGG	240
CTATTGGCCA TTGCATACGT TGTATCCATA TCATAATATG TACATTTATA TTGGCTCATG	300
TCCAACATTA CCGCCATGTT GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC	360
GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCGCGTT ACATAACTTA CGGTAAATGG	420
CCCGCCTGGC TGACCGCCCA ACGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC	480
CATAGTAACG CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC	540
TGCCCCACTTG GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA TTGACGTCAA	600
TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG ACCTTATGGG ACTTTCCTAC	660
TTGGCAGTAC ATCTACGTAT TAGTCATCGC TATTACCATG GTGATGCGGT TTTGGCAGTA	720
CATCAATGGG CGTGGATAGC GGTTTGACTC ACGGGGATTT CCAAGTCTCC ACCCCATTGA	780
CGTCAATGGG AGTTTGT TTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA	840
CTCCGCCCCA TTGACGCAAA TGGGCGGTAG GCGTGACGG TGGGAGGTCT ATATAAGCAG	900

AGCTCGTTTA GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT TTGACCTCCA	960
TAGAAGACAC CGGGACCGAT CCAGCCTCCG CGGCCGGGAA CGGTGCATTG GAACGCGGAT	1020
TCCCCGTGCC AAGAGTGACG TAAGTACCGC CTATAGAGTC TATAGGCCCA CCCCCTTGGC	1080
TTCTTATGCA TGCTATACTG TTTTGGCTT GGGGTCTATA CACCCCCGCT TCCTCATGTT	1140
ATAGGTGATG GTATAGCTTA GCCTATAGGT GTGGGTATT GACCATTATT GACCACTCCC	1200
CTATTGGTGA CGATACTTTC CATTACTAAT CCATAACATG GCTCTTTGCC ACAACTCTCT	1260
TTATTGGCTA TATGCCAATA CACTGTCCTT CAGAGACTGA CACGGACTCT GTATTTTAC	1320
AGGATGGGGT CTCATTTATT ATTTACAAAT TCACATATAC AACACCACCG TCCCCAGTGC	1380
CCGCAGTTTT TATTAAACAT AACGTGGGAT CTCCACGCGA ATCTCGGGTA CGTGTTCGGG	1440
ACATGGGCTC TTCTCCGGTA GCGGCGGAGC TTCTACATCC GAGCCCTGCT CCCATGCCTC	1500
CAGCGACTCA TGGTCGCTCG GCAGCTCCTT GCTCCTAACA GTGGAGGCCA GACTTAGGCA	1560
CAGCACGATG CCCACCACCA CCAGTGTGCC GCACAAGGCC GTGGCGGTAG GGTATGTGTC	1620
TGAAAATGAG CTCGGGGAGC GGGCTTGCAC CGCTGACGCA TTTGGAAGAC TTAAGGCAGC	1680
GGCAGAAGAA GATGCAGGCA GCTGAGTTGT TGTGTTCTGA TAAGAGTCAG AGGTAACTCC	1740
CGTTGCGGTG CTGTTAACGG TGGAGGGCAG TGTAGTCTGA GCAGTACTCG TTGCTGCCGC	1800
GCGCGCCACC AGACATAATA GCTGACAGAC TAACAGACTG TTCCTTTCCA TGGGTCTTTT	1860
CTGCAGTCAC CGTCCTTAGA TCTGCTGTGC CTTCTAGTTG CCAGCCATCT GTTGTTTGCC	1920
CCTCCCCCGT GCCTTCCTTG ACCCTGGAAG GTGCCACTCC CACTGTCCTT TCCTAATAAA	1980
ATGAGGAAAT TGCATCGCAT TGTCTGAGTA GGTGTCATTC TATTCTGGGG GGTGGGGTGG	2040
GGCAGCACAG CAAGGGGGAG GATTGGGAAG ACAATAGCAG GCATGCTGGG GATGCGGTGG	2100
GCTCTATGGG TACCCAGGTG CTGAAGAATT GACCCGGTTC CTCCTGGGCC AGAAAGAAGC	2160
AGGCACATCC CCTTCTCTGT GACACACCCT GTCCACGCCC CTGGTTCTTA GTTCCAGCCC	2220
CACTCATAGG AACTCATAG CTCAGGAGGG CTCCGCCTTC AATCCCACCC GCTAAAGTAC	2280
TTGGAGCGGT CTCTCCCTCC CTCATCAGCC CACCAAACCA AACCTAGCCT CCAAGAGTGG	2340
GAAGAAATTA AAGCAAGATA GGCTATTAAG TGCAGAGGGA GAGAAAATGC CTCCAACATG	2400
TGAGGAAGTA ATGAGAGAAA TCATAGAATT TCTTCCGCTT CCTCGCTCAC TGA CTGCTG	2460
CGCTCGGTGCG TTCGGCTGCG GCGAGCGGTA TCAGCTCACT CAAAGGCGGT AATACGGTTA	2520
TCCACAGAAT CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAGGCC	2580

AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	2640
CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2700
CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	2760
GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	2820
AGGTATCTCA	GTTGCGTGTA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	2880
GTTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	AACTATCGTC	TTGAGTCCAA	CCCGGTAAGA	2940
CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	3000
GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	AAGGACAGTA	3060
TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	3120
TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	3180
CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	TGACGCTCAG	3240
TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG	GATCTTCACC	3300
TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	TGAGTAAACT	3360
TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	3420
CGTTCATCCA	TAGTTGCCTG	ACTCCGGGGG	GGGGGGGCGC	TGAGGTCTGC	CTCGTGAAGA	3480
AGGTGTTGCT	GACTCATACC	AGGCCTGAAT	CGCCCCATCA	TCCAGCCAGA	AAGTGAGGGA	3540
GCCACGGTTG	ATGAGAGCTT	TGTTGTAGGT	GGACCAGTTG	GTGATTTTGA	ACTTTTGCTT	3600
TGCCACGGAA	CGGTCTGCGT	TGTCGGGAAG	ATGCGTGATC	TGATCCTTCA	ACTCAGCAAA	3660
AGTTTCGATTT	ATTCAACAAA	GCCGCCGTCC	CGTCAAGTCA	GCGTAATGCT	CTGCCAGTGT	3720
TACAACCAAT	TAACCAATTC	TGATTAGAAA	AACTCATCGA	GCATCAAATG	AAACTGCAAT	3780
TTATTCATAT	CAGGATTATC	AATACCATAT	TTTTGAAAAA	GCCGTTTCTG	TAATGAAGGA	3840
GAAAACCTCAC	CGAGGCAGTT	CCATAGGATG	GCAAGATCCT	GGTATCGGTC	TGCGATTCCG	3900
ACTCGTCCAA	CATCAATACA	ACCTATTAAT	TTCCCCTCGT	CAAAAATAAG	GTTATCAAGT	3960
GAGAAATCAC	CATGAGTGAC	GACTGAATCC	GGTGAGAATG	GCAAAAGCTT	ATGCATTTCT	4020
TTCCAGACTT	GTTCAACAGG	CCAGCCATTA	CGCTCGTCAT	CAAAATCACT	CGCATCAACC	4080
AAACCGTTAT	TCATTCGTGA	TTGCGCCTGA	GCGAGACGAA	ATACGCGATC	GCTGTAAAAA	4140
GGACAATTAC	AAACAGGAAT	CGAATGCAAC	CGGCGCAGGA	ACACTGCCAG	CGCATCAACA	4200
ATATTTTCAC	CTGAATCAGG	ATATTCTTCT	AATACCTGGA	ATGCTGTTTT	CCCGGGGATC	4260

GCAGTGGTGA GTAACCATGC ATCATCAGGA GTACGGATAA AATGCTTGAT GGTCGGAAGA	4320
GGCATAAAATT CCGTCAGCCA GTTTAGTCTG ACCATCTCAT CTGTAACATC ATTGGCAACG	4380
CTACCTTTGC CATGTTTCAG AAACAACTCT GGCGCATCGG GCTTCCCATA CAATCGATAG	4440
ATTGTCGCAC CTGATTGCCC GACATTATCG CGAGCCCATT TATACCCATA TAAATCAGCA	4500
TCCATGTTGG AATTTAATCG CGGCCTCGAG CAAGACGTTT CCCGTTGAAT ATGGCTCATA	4560
ACACCCCTTG TATTACTGTT TATGTAAGCA GACAGTTTTA TTGTTCATGA TGATATATTT	4620
TTATCTTGTG CAATGTAACA TCAGAGATTT TGAGACACAA CGTGGCTTTC CCCCCCCCCC	4680
CATTATTGAA GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT	4740
TAGAAAAATA AACAAATAGG GGTTCCGCGC ACATTTCCCC GAAAAGTGCC ACCTGACGTC	4800
TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAATA GGCGTATCAC GAGGCCCTTT	4860
CGTC	4864

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAGAAGCA GAGCA

15

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCACCGTCCT TAGATCAAGC AGGGTTAATA ATCACTCACT GAGTGACATC AAAATCATGG 60

CGTCCCAAGG CACCAAACGG TCTTATGAAC AGATGGAAAC TGATGGGGAA CGCCAGATT 119

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGGGGCAAA CAACAGATGG CTGGCAACTA GAAGGCACAG CAGATATTTT TTCCTTAATT 60

GTCGTAC 67

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCAGAAGCA CGCAC 15

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCAGAAGCA CAGCA

15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCTTAGATCG GAAATAAAAA CAACCAAAAT GAA

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAGATCCTT ATATTCTGA AATTCTGGTC TCAGAT

36

(2) INFORMATION FOR SEQ ID NO:26:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACCGTCCTTA GATCCAGAAG CAGAGCATTT TCTAATATCC ACAAATGAA GGCAATAATT	60
GTACTACTCA TGGTAGTAAC ATCCAACGCA GATCGAATCT GC	102

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGCACAGCAG ATCTTTCAAT AACGTTTCTT TGTAATGGTA AC	42
--	----

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAACAGACT GTTCCTTTCC ATG

23

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGAGTGGCAC CTTCCAGG

18

(2) INFORMATION FOR SEQ ID NO:30:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCAAAAGCA GG

12

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGCAGAAGCG GAGC

14

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCACATGTCG ACCCGTAAAA AGGCCGCGTT GCTGG

35

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGTACAACCA TGAAGACTAT CATTGCTTTG AGC

33

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCACATAGAT CTTCAAATGC AAATGTTGCA CCTAATG

37

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTACAACCA TGAAAGCAAA ACTACTAGTC CTGTTATG

38

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCACATTCAG ATGCATATTC TAACTGCAA AG

32

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTACAACCA TGAAGGCAAT AATTGTACTA CTCATG

36

(2) INFORMATION FOR SEQ ID NO:38:

- (1) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCACATTTAT AGACAGATGG AGCAAGAAAC ATTGTC

36

(2) INFORMATION FOR SEQ ID NO:39:

- (1) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGTACAAGAT CTACCATGCT TCTAACCGAG GTC

33

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCACATAGAT CTTCACTTGA ACCGTTGCAT CTGCAC

36

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGTACAGGAT CCACCATGTC CAACATGGAT ATTGACGGC

39

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCACATGGAT CCTTAATAAT CGAGGTCATC ATAATCCTC

39

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGTACAGGAT CCACCATGTC GCTGTTTGGG GACACAATTG CC

42

## (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCACATGGAT CCTTATAGGT ATTTCTTCAC AAGAGCTG

38

## (2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3553 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATATTGGCT ATTGGCCATT GCATACGTTG TATCCATATC ATAATATGTA CATTTATATT	60
GGCTCATGTC CAACATTACC GCCATGTTGA CATTGATTAT TGACTAGTTA TTAATAGTAA	120
TCAATTACGG GGTCAATTAGT TCATAGCCCA TATATGGAGT TCCGCGTTAC ATAACCTTACG	180
GTAAATGGCC CGCCTGGCTG ACCGCCCAAC GACCCCCGCC CATTGACGTC AATAATGACG	240
TATGTTCCCA TAGTAACGCC AATAGGGACT TTCCATTGAC GTCAATGGGT GGAGTATTTA	300
CGGTAAACTG CCCACTTGGC AGTACATCAA GTGTATCATA TGCCAAGTAC GCCCCCTATT	360
GACGTCAATG ACGGTAAATG GCCCGCCTGG CATTATGCCC AGTACATGAC CTTATGGGAC	420
TTTCCTACTT GGCAGTACAT CTACGTATTA GTCATCGCTA TTACCATGGT GATGCGGTTT	480
TGGCAGTACA TCAATGGGCG TGGATAGCGG TTTGACTCAC GGGGATTTCC AAGTCTCCAC	540
CCCATTGACG TCAATGGGAG TTTGTTTTGG CACCAAAATC AACGGGACTT TCCAAAATGT	600
CGTAACAAC TCCGCCCATC GACGCAAATG GGCGGTAGGC GTGTACGGTG GGAGGTCTAT	660
ATAAGCAGAG CTCGTTTAGT GAACCGTCAG ATCGCCTGGA GACGCCATCC ACGCTGTTTT	720
GACCTCCATA GAAGACACCG GGACCGATCC AGCCTCCGCG GCCGGGAACG GTGCATTGGA	780
ACGCGGATTC CCCGTGCCAA GAGTGACGTA AGTACCGCCT ATAGAGTCTA TAGGCCCACC	840
CCCTTGGCTT CTTATGCATG CTATACTGTT TTTGGCTTGG GGTCTATACA CCCCCGCTTC	900
CTCATGTTAT AGGTGATGGT ATAGCTTAGC CTATAGGTGT GGGTTATTGA CCATTATTGA	960
CCACTCCCCT ATTGGTGACG ATACTTTCCA TTACTAATCC ATAACATGGC TCTTTGCCAC	1020
AACTCTCTTT ATTGGCTATA TGCCAATACA CTGTCCTTCA GAGACTGACA CGGACTCTGT	1080
ATTTTACAG GATGGGGTCT CATTTATTAT TTACAAATC ACATATACAA CACCACCGTC	1140
CCCAGTGCCC GCAGTTTTTA TTAAACATGC TAACGTGGGA TCTCCACGCG AATCTCGGGT	1200
ACGTGTTCCG GACATGGGCT CTTCTCCGGT AGCGGCGGAG CTTCTACATC CGAGCCCTGC	1260
TCCCATGCCT CCAGCGACTC ATGGTCGCTC GGCAGCTCCT TGCTCCTAAC AGTGAGGGCC	1320
AGACTTAGGC ACAGCACGAT GCCCACCACC ACCAGTGTGC CGCACAAGGC CGTGGCGGTA	1380
GGGTATGTGT CTGAAAATGA GCTCGGGGAG CGGGCTTGCA CCGCTGACGC ATTTGGAAGA	1440
CTTAAGGCAG CGGCAGAAGA AGATGCAGGC AGCTGAGTTG TTGTGTTCTG ATAAGAGTCA	1500
GAGGTAAGTC CCGTTGCGGT GCTGTTAACG GTGGAGGGCA GTGTAGTCTG AGCAGTACTC	1560
GTTGCTGCCG CGCGCGCCAC CAGACATAAT AGCTGACAGA CTAACAGACT GTTCCTTTCC	1620

ATGGGTCTTT TCTGCAGTCA CCGTCCTTAG ATCTGCTGTG CCTTCTAGTT GCCAGCCATC 1680  
 TGTGTTTTGC CCCTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCCT 1740  
 TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT CTATTCTGGG 1800  
 GGGTGGGGTG GGGCAGCACA GCAAGGGGGA GGATTGGGAA GACAATAGCA GGCATGCTGG 1860  
 GGATGCGGTG GGCTCTATGG GTACGGCCGC AGCGGCCGTA CCCAGGTGCT GAAGAATTGA 1920  
 CCCGGTTCCT CGACCCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG GCTCCGCCCC 1980  
 CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT GGCGAAACCC GACAGGACTA 2040  
 TAAAGATACC AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG 2100  
 CCGCTTACCG GATACCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC 2160  
 TCACGCTGTA GGTATCTCAG TTCGGTGTAG GTCGTTTCGCT CCAAGCTGGG CTGTGTGCAC 2220  
 GAACCCCCCG TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC 2280  
 CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG GTAACAGGAT TAGCAGAGCG 2340  
 AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC CTAACACGG CTACACTAGC 2400  
 TGAAGGACAG TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT 2460  
 GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTGCAAG 2520  
 CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGTGA 2580  
 TCCCGTAATG CTCTGCCAGT GTTACAACCA ATTAACCAAT TCTGATTAGA AAAACTCATC 2640  
 GAGCATCAAA TGAAACTGCA ATTTATTCAT ATCAGGATTA TCAATACCAT ATTTTTGAAA 2700  
 AAGCCGTTTC TGTAATGAAG GAGAAAACTC ACCGAGGCAG TTCCATAGGA TGGCAAGATC 2760  
 CTGGTATCGG TCTGCGATTC CGACTCGTCC AACATCAATA CAACCTATTA ATTTCCCCTC 2820  
 GTCAAAAATA AGGTTATCAA GTGAGAAATC ACCATGAGTG ACGACTGAAT CCGGTGAGAA 2880  
 TGGCAAAAGC TTATGCATTT CTTTCCAGAC TTGTTCAACA GGCCAGCCAT TACGCTCGTC 2940  
 ATCAAAATCA CTCGCATCAA CCAAACCGTT ATTCATTCTG GATTGCGCCT GAGCGAGACG 3000  
 AAATACGCGA TCGCTGTAA AAGGACAATT ACAAACAGGA ATCGAATGCA ACCGGCGCAG 3060  
 GAACACTGCC AGCGCATCAA CAATATTTTC ACCTGAATCA GGATATTCTT CTAATACCTG 3120  
 GAATGCTGTT TTCCCGGGGA TCGCAGTGGT GAGTAACCAT GCATCATCAG GAGTACGGAT 3180  
 AAAATGCTTG ATGGTCGGAA GAGGCATAAA TTCCGTCAGC CAGTTTAGTC TGACCATCTC 3240  
 ATCTGTAACA TCATTGGCAA CGCTACCTTT GCCATGTTTC AGAAACAACCT CTGGCGCATC 3300

GGGCTTCCCA TACAATCGAT AGATTGTCGC ACCTGATTGC CCGACATTAT CGCGAGCCCA 3360  
 TTTATACCCA TATAAATCAG CATCCATGTT GGAATTTAAT CGCGGCCTCG AGCAAGACGT 3420  
 TTCCCGTTGA ATATGGCTCA TAACACCCCT TGTATTACTG TTTATGTAAG CAGACAGTTT 3480  
 TATTGTTTAT GATGATATAT TTTTATCTTG TGCAATGTAA CATCAGAGAT TTTGAGACAC 3540  
 AACGTGGCTT TCC 3553

## (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCACCGTCCT TAGATCGGTA CAACCATGAA GACTATCATT GCTTTGAGCT ACATTTTATG 60  
 TCTGGTTTTC GC 72

## (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCATGCTTTT TGCTTTGTGT TGTTTTGCTG GGGTTCATCA TGTGGGCCTG CCAAAAAGGC 60  
 AACATTAGGT GCAACATTTG CATTTGAAGA TCTATGTGGG ATCTGCTGTG C 111

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TTAGATCGGA ACATGAAAGC AAAACTACTA GTCCTGTTAT GTGCATTAC AGCTACATAT	60
GCA	63

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGGTGCTTT TGGTCTCCCT GGGGCAATC AGCTTCTGGA TGTGTTCTAA TGGGTCTTTG	60
CAGTGTAGAA TATGCATCTG AATGTGGGAT CTGCTGTGCC TT	102

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCTTAGATCG GTACAACCAT GAAGGCAATA ATTGTACTAC TCATGGTAGT AACATCCAAC 60  
 GCAGATCGAA TCTGCACTGG GATAACATCT TCAAACCTCAC CTCATGTG 108

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTGGCTGTAA CATTGATGAT AGCTATTTTT ATTGTTTATA TGGTCTCCAG AGACAATGTT 60  
 TCTTGCTCCA TCTGTCTATA AATGTGGGAT CTGCTGTGCC TT 102

## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTCCTTAGAT CCACCATGGC GTCCCAAGGC ACCAAACGGT CTTATGAACA GATGGAAACT 60  
 GATGGGGAAC GCCAGAATGC AACT 84

## (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAAAAGGCAA CGAACCCGAT CGTGCCCTCT TTTGACATGA GTAATGAAGG ATCTTATTTT	60
TTCGGAGACA ATGCAGAAGA GTACGACAAT TAAGGATCTG CTGTGCCT	108

(2) INFORMATION FOR SEQ ID NO:54

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTTAGATCCA GATCTACCAT GAGTCTTCTA ACCGAGGTCG AAACGTATGT TCTCTCTATC	60
GTTCCATCAG GCCCCCTCAA AGCCGAAATC GCGCAGAGAC TTGAAGATGT CTTTGCTGGG	120
AAAAACACAG AT	132

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 129 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  
 GGGACTCATC CTAGCTCCAG TACTGGTCTA AAAGATGATC TTCTTGAAAA TTTGCAGACC 60  
 TATCAGAAAC GAATGGGGGT GCAGATGCAA CGGTTCAAGT GAAGATCTAT GTGGGATCTG 120  
 CTGTGCCTT 129

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 81 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  
 CTTAGATCCA CCATGTCCAA CATGGATATT GACGGTATCA AACTGGGAC AATTGACAAA 60  
 ACACCGGAAG AAATAACTTC T 81

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:  
 GTTGAAATTC CAATTAAGCA GACCATCCCC AATTTCTTCT TTGGGAGGGA CACAGCAGAG 60  
 GATTATGATG ACCTCGATTA TTAAGGATCT GCTGTG 96

(2) INFORMATION FOR SEQ ID NO:58:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTTAGATCCA CCATGTCGCT GTTTGGAGAC ACAATTGCCT ACCTGCTTTC ATTGACAGAA 60

GATGGAGAAG GCAAAGCAGA ACTAGCAGAA AAATTA 96

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGATCTCTTG GGGCAAGTCA AGAGAATGGG GAAGGAATTG CAAAGGATGT GATGGAAGTG 60

CTAAAGCAGA GCTCTATGGG AAATTCAGCT CTTGTGAAGA AATACCTATA AGGATCTGCT 120

GTG 123

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGTACAAATA TTGGCTATTG GCCATTGCAT ACG

33

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCACATCTCG AGGAACCGGG TCAATTCTTC AGCACC

36

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGTACAGATA TCGGAAAGCC ACGTTGTGTC TCAAAATC

38

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCACATGGAT CCGTAATGCT CTGCCAGTGT TACAACC

37

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGTACATGAT CACGTAGAAA AGATCAAAGG ATCTTCTTG

39